



STIC Search Report

Biotech-Chem Library

File Copy
09/747, 385
update

STIC Database Tracking Number: 141924

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Thursday, January 06, 2005

Case Serial Number: 09/747385

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David
Sent: Wednesday, January 05, 2005 9:15 AM
To: O'Bryen, Barbara; Fredman, Jeffrey
Subject: RE: problem re: us09747385

Yes, I apologize for not indicating that...please cancel the oligomer search portion. In retrospect, it appears I should not have included it in the first place.

Dave.

-----Original Message-----

From: O'Bryen, Barbara
Sent: Wednesday, January 05, 2005 9:14 AM
To: Fredman, Jeffrey
Cc: Lambertson, David
Subject: FW: problem re: us09747385

Jeff,

I'll let you know the new processing times when I set up the search. What you've recommended will definitely reduce the processing time. I have one question - has the oligomer portion of the search request been cancelled, or should I also do an oligomer search on the selected fragments.

Thanks,
Barb

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 8:42 AM
To: O'Bryen, Barbara
Subject: FW: problem re: us09747385

Barb,

Here is what Jeff recommended as far as improving the search. Let me know if there is anything else you need from me.

THanks a bunch,
Dave.

-----Original Message-----

From: Fredman, Jeffrey
Sent: Wednesday, January 05, 2005 7:58 AM
To: Lambertson, David
Subject: RE: problem re: us09747385

David,

I looked at the case and it is clear that for SEQ ID NOs: 6 and 15, you really only need to search a small part to see if they are out there. Since the claims are comprising and no fragments are claimed, a perfect match is essentially required. So a search of each end of the DNAs would tell you if there are any perfect hits. If there are any, it is very easy for stic to align one or two hits with the sequence at issue.

So I would recommend search nucleotides 1-250 and 9700-9955 of SEQ ID NO: 15 only. For SEQ ID NO: 6, search nucleotides 1-250 and nucleotides 5600-5887 or so. This search will run somewhat faster (If Barb could let me know how much, I would really appreciate it).

Jeff Fredman

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 6:57 AM
To: Fredman, Jeffrey

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2591.45 Seconds
 (without alignment) 4049.721 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agccaatccaaaaataata.....atcatctaaatcttaatt 288

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : EST:
 1: gb_est1:
 2: gb_est2:
 3: gb_htc:
 4: gb_pct3:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_gss1:
 9: gb_gss2:
 *:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	92.6	32.2	1119	9	AG376945		AG376945 Mus musculus
2	91.8	31.9	889	9	CNS006W4		AL065939 Drosophila
c 3	91.4	31.7	951	8	AZ676519		AZ676519 ENTRGV5TF
c 4	89	30.9	889	9	CNS006W4		AL065939 Drosophila
c 5	88.4	30.7	417	9	CNS02AH7		AL188548 Tetradon
c 6	88.4	30.7	1221	9	AG360812		AG360812 Mus musculus
c 7	88.2	30.6	951	8	AZ676519		AZ676519 ENTRGV5TF
c 8	87.4	30.3	613	8	AQ922590		AQ922590 RPCI-23-2
c 9	86.8	30.1	1119	9	AG376945		AG376945 Mus musculus
10	86.4	30.0	613	8	AQ922590		AQ922590 RPCI-23-2
11	85.8	29.8	417	9	CNS02AH7		BH163549 ENTRGV8TR
c 12	85.6	29.7	939	8	BH163549		AL288309 Tetradon
c 13	85.2	29.6	433	9	CNS04FGC		CL142825 ISB1-120N
c 14	85.2	29.6	1101	9	CNS001L2		CL142825 ISB1-120N
15	84.6	29.4	1295	9	CG757539		CL142825 ISB1-120N
16	84.2	29.2	1263	9	AG396942		CL142825 ISB1-120N
17	84	29.2	868	8	AZ673655		CL142825 ISB1-120N
c 18	83.8	29.1	875	9	CL142825		CL142825 ISB1-120N
c 19	83.2	28.9	875	9	CL03318		CL03318 CH216-36F
c 20	83.2	28.9	1275	9	CF872119		CF872119 tric029xp
21	82.8	28.7	706	7	CF872119		BH163549 ENTRGV8TR
22	82.6	28.7	939	8	CD049544		CD049544 AGENCOURT
23	82.6	28.7	997	9	CNS04FGC		AL288309 Tetradon
24	82.4	28.6	433	9	CNS04FGC		

FEATURES

Source	Location/Qualifiers
	1..1119
	/organism="Mus musculus molossinus"
	/mol_type="genomic DNA"
	/sub_species="molossinus"
	/db_xref="taxon:514785"
	/clone="MSMG01-184M01-T7"
	/sex="male"
	/tissue_type="mixture of kidney and spleen"
	/clone_id="MSMG01 Mouse Male BAC Library"

Result No.	Score	Query Match	Length	DB ID	Description
C 1	76.2	26.5	3673778	15	US-10-312-841-2
C 2	75.8	26.3	10039	15	US-10-311-455-883
C 3	72.6	25.2	585	18	US-10-424-599-79137
C 4	69.8	24.2	5908	14	US-09-960-352-2699
C 5	69.8	24.2	5908	15	US-10-357-930-58133
C 6	69.8	24.2	5908	16	US-10-312-841-1
C 7	69.6	24.2	6486	17	US-10-433-793-80
C 8	68.6	23.8	529	18	US-10-425-115-171364
C 9	68.6	23.8	543	17	US-10-321-333-14156
C 10	68.2	23.7	433	10	US-09-918-993-4250
C 11	67.8	23.5	474	18	US-10-425-115-2807
C 12	67.8	23.5	545	16	US-10-324-599-142212

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	76.2	26.5	3673778	15	US-10-312-841-2
C 2	75.8	26.3	10039	15	Sequence 2, Appli
C 3	72.6	25.2	585	18	Sequence 2015, Appli
C 4	69.8	24.2	5908	14	Sequence 58104, Appli
C 5	69.8	24.2	5908	15	Sequence 93, Appli
C 6	69.8	24.2	5908	16	Sequence 105, Appli
C 7	69.6	24.2	6486	17	Sequence 175, Appli
C 8	68.6	23.8	529	18	Sequence 80, Appli
C 9	68.6	23.8	543	17	Sequence 17156,
C 10	68.2	23.7	433	10	Sequence 14156, Appli
C 11	67.8	23.5	474	18	Sequence 4250, Appli
C 12	67.8	23.5	545	16	Sequence 2807, Appli

RESULT 1
US-10-312-841-2/c
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb
; FILE REFERENCE: E01:12081WO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

ALIGNMENTS

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 17156,	17156		
Sequence 14156, Appli	14156		
Sequence 4250, Appli	4250		
Sequence 2807, Appli	2807		
Sequence 17156, Appli	17156		
Sequence 14156, Appli	14156		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 105, Appli	105		
Sequence 93, Appli	93		
Sequence 58104, Appli	58104		
Sequence 2015, Appli	2015		
Sequence 2, Appli	2		
Sequence 1, Appli	1		

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCES

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 17156,	17156		
Sequence 14156, Appli	14156		
Sequence 4250, Appli	4250		
Sequence 2807, Appli	2807		
Sequence 17156, Appli	17156		
Sequence 14156, Appli	14156		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 105, Appli	105		
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Sequence 58104, Appli	58104		
Sequence 2015, Appli	2015		
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Sequence 2015, Appli	0	Mismatches	123;
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Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 17156,	17156		
Sequence 14156, Appli	14156		
Sequence 4250, Appli	4250		
Sequence 2807, Appli	2807		
Sequence 17156, Appli	17156		
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Sequence 175, Appli	175		
Sequence 105, Appli	105		
Sequence 93, Appli	93		
Sequence 58104, Appli	58104		
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Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
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Sequence 175, Appli	175		
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Sequence 58104, Appli	58104		
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Sequence 1, Appli	1		

SEQUENCES

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Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
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Sequence 14156, Appli	14156		
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Sequence 105, Appli	105		
Sequence 93, Appli	93		
Sequence 58104, Appli	58104		
Sequence 2015, Appli	2015		
Sequence 2, Appli	2		
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SEQUENCES

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
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Sequence 93, Appli	93		
Sequence 58104, Appli	58104		
Sequence 2015, Appli	2015		
Sequence 2, Appli	2		
Sequence 1, Appli	1		

SEQUENCES

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
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Sequence 58104, Appli	58104		
Sequence 2015, Appli	2015		
Sequence 2, Appli	2		
Sequence 1, Appli	1		

SEQUENCES

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
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Sequence 17156,	17156		
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Sequence 93, Appli	93		
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Sequence 2, Appli	2		
Sequence 1, Appli	1		

SEQUENCES

Query Match	Length	DB ID	Description
Sequence 2, Appli	54.9t	Pred. No. 0	0.065;
Sequence 2015, Appli	0	Mismatches	123;
Sequence 58104, Appli	93	Indels	0;
Sequence 93, Appli	105	Gaps	0;
Sequence 105, Appli	175		
Sequence 80, Appli	80		
Sequence 175, Appli	175		
Sequence 17156,	17156		
Sequence 14156, Appli	14156		
Sequence 4250, Appli	4250		
Sequence 2807, Appli	2807		
Sequence 17			

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 64.5517 Seconds
 (without alignments)
 3171.212 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatccaaaaataaa.....atcatctaaatctttaaaatt 288

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents NA:
 1: /cgn2_6/pcodata/1/ina/5A_COMB.seq;
 2: /cgn2_6/pcodata/1/ina/5B_COMB.seq;
 3: /cgn2_6/pcodata/1/ina/6A_COMB.seq;
 4: /cgn2_6/pcodata/1/ina/6B_COMB.seq;
 5: /cgn2_6/pcodata/1/ina/PECTUS.seq;
 6: /cgn2_6/pcodata/1/ina/backfiles1.seq; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71.2	24.7	196	4	US-09-442-054A-42
c 2	71.2	24.7	196	4	US-09-442-054A-42
c 3	59.6	20.4	731	1	Sequence 42, App1
c 4	58.8	20.4	5852	1	Sequence 42, App1
c 5	58.4	20.3	2621	2	Sequence 42, App1
c 6	56.4	19.6	8607	4	Sequence 42, App1
c 7	56.4	19.6	1664976	4	Sequence 42, App1
8	56.4	19.6	1577	4	Sequence 42, App1
9	56.2	19.5	1577	4	Sequence 42, App1
10	56.2	19.5	1577	4	Sequence 42, App1
c 11	55.8	19.4	20674	4	Sequence 42, App1
c 12	55.8	19.4	20674	4	Sequence 42, App1
c 13	55	19.1	6243	2	Sequence 42, App1
c 14	54.6	19.0	3138	1	Sequence 42, App1
c 15	54	18.8	3440	1	Sequence 42, App1
c 16	54	18.8	3440	5	Sequence 42, App1
c 17	53.6	18.6	8607	4	Sequence 42, App1
c 18	52.8	18.3	5455	4	Sequence 42, App1
c 19	52.6	18.3	731	1	Sequence 42, App1
c 20	52.6	18.3	2146	4	Sequence 42, App1
c 21	52.6	18.3	3275	4	Sequence 42, App1
c 22	52.6	18.3	3275	4	Sequence 42, App1
c 23	52.4	18.2	6079	4	Sequence 42, App1
c 24	52.4	18.2	10619	4	Sequence 42, App1
c 25	52.4	18.2	1738	4	Sequence 42, App1
c 26	52.2	18.1	3138	1	Sequence 42, App1
c 27	52.2	18.1	3138	1	Sequence 42, App1

RESULTS

SEQ ID	SEQUENCE	TYPE	ORGANISM	FEATURE	OTHER INFORMATION	CURRENT FILING DATE	PRIOR APPLICATION NUMBER	PRIOR FILING DATE	PRIOR APPLICATION NUMBER	PRIOR FILING DATE	FILE REFERENCE	CURRENT APPLICATION NUMBER	PRIOR FILING DATE	PRIOR APPLICATION NUMBER	PRIOR FILING DATE	NUMBER OF SEQ ID NOs:	SOFTWARE: PatentIn version 3.1	
1	US-09-442-054A-42	DNA	Artificial Sequence			2002-05-07	US-09-442-054A-42	1995-06-07	US-09-442-054A-42	1993-04-26	ISIS290	US-09-442-054A-42	1995-06-07	US-09-442-054A-42	1993-04-26	89	SEQ ID NO 42	
																		Length: 196;
																		PATENT INFORMATION:
																		Patent No. 67707298
																		GENERAL INFORMATION:
																		APPLICANT: Ecker, David J.
																		APPLICANT: Buchardt, Ole
																		APPLICANT: Egholm, Michael
																		APPLICANT: Berg, Rolf H.
																		APPLICANT: Mollegaard, Neils E.
																		TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
																		CURRENT FILING DATE: 2002-05-07
																		PRIOR FILING DATE: 1995-06-07
																		MISMATCHES: 0;
																		INDELS: 0;
																		GAPS: 0;

ALIGNMENTS

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 304.828 Seconds

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288 (without alignments)

Sequence: 1 agtcaataaaaataaa.....atcatctaaatcttaatt 288

4959.634 Million cell updates/sec

Scoring table: IDENTITY_NUC Gapov 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 82659772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseqn23Sep04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	84.4	29.3	435	4	AAI82079		Aai82079 Human pol
c 2	75.8	26.3	10039	6	ABL34042		Abi34042 Human imm
c 3	72.8	25.3	380	4	AAI80554		Aai80354 Human pol
c 4	72.6	25.2	585	5	ABV58085		Abv58085 Human pro
c 5	69.8	24.2	5908	4	AAS45316		Aas45316 Chemical
c 6	69.8	24.2	5908	6	ABK28231		Abk28231 DNA trans
c 7	69.8	24.2	5908	6	AAS61216		Aas61216 Human gen
c 8	69.6	24.2	6486	6	ABQ67050		Abq67050 Human ang
c 9	69	24.0	364	4	AAI84912		Aai84912 Human pol
10	68.2	23.7	433	9	ACH17038		Ach17038 Human adu
11	67.2	23.3	8946	6	ABL32910		Abi32910 Human imm
12	66.8	23.2	435	8	ABX37534		Abx37534 Bovine ES
13	66.6	23.1	361	4	AAI85535		Aai85535 Human pol
14	66.6	23.1	510	5	ABV58114		Abv58114 Human pro
15	66.4	23.1	461	5	ABD418834		Adi418834 Human ova
c 16	66.2	23.0	423	9	ACH17038		Ach17038 Human imm
c 17	66	22.9	6436	6	ABL32881		Abi32881 Human imm
c 18	65.8	22.8	1543	8	ACC72157		Acc72157 Human NOV
c 19	65.8	22.8	6162	6	ABK31331		Abk31331 Signal tr
c 20	65.4	22.7	317	5	ABV58181		Abv58181 Human pro
c 21	65.4	22.7	603	5	ABV58645		Abv58645 Human pro

ALIGNMENTS

RESULT 1							
ID	AAI82079	standard	cdNA;	435	BP.		
XX	XX						
AC	AAI82079;						
XX	XX						
DT	06-NOV-2001	(first entry)					
XX	XX						
DE	Human polynucleotide SEQ ID NO 2139.						
XX	XX						
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.						
XX	XX						
OS	Home sapiens.						
XX	XX						
PN	WO200164835-A2.						
XX	XX						
PD	07-SEP-2001.						
XX	XX						
PF	26-FEB-2001; 2001WO-US004927.						
XX	XX						
PR	28-FEB-2000; 2000US-00515126.						
PR	18-MAY-2000; 2000US-00577409.						
PA	(HYSE-) HYSEQ INC.						
XX	XX						
PI	Tang YT, Liu C, Drmanac RT;						
XX	XX						
DR	WPI; 2001-514838/56.						
DR	P-NSDB; AAO2148.						
XX	XX						
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.						
XX	XX						
PS	Claim 1; SEQ ID NO 2139; 139pp + Sequence Listing; English.						
XX	XX						
CC	The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA01310) that exhibit activity eliciting to						
CC	cytokine, cell proliferation or cell differentiation or which may induce						
CC	production of other cytokines in other cell populations. The						
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or						
CC	peptide therapy. The polypeptides have various cytokine-like activities,						

Database :	GenEmbl::*	ALIGNMENTS									
	1: gb ba:*	RESULT 1	AF159249	LOCUS	AF159249	5887 bp	DNA	circular BCT 09-FEB-2000			
	2: gb_htg:*	DEFINITION	Fusobacterium nucleatum plasmid pFN1, complete sequence.	ACCESSION	AF159249						
	3: gb_in:*	VERSION	AF159249.1	GI	:6941824						
	4: gb_om:*	KEYWORDS		SOURCE							
	5: gb_ov:*			ORGANISM							
	6: gb_Pat:*			Bacteria; Fusobacteria; Fusobacteriaceae;							
	7: gb_ph:*			Fusobacterium							
	8: gb_Dl:*			nucleatum							
	9: gb_Dr:*			Bacterium							
	10: gb_ro:*			nucleatum							
	11: gb_sts:*			Fusobacterium							
	12: gb_sy:*			nucleatum							
	13: gb_un:*			Transformation of Fusobacterium nucleatum by electroporation							
	14: gb_vl:*			(Abstract #H-9)							
				Abstr. Gen. Meet. Am. Soc. Microbiol.	99,	331	(1999)				
				JOURNAL	3	(bases 1 to 5887)					
				REFERENCE							
				AUTHORS	Kinder Haake, S., Yoder, S.C., Attaran, G., and Podkaminer, K.						
				TITLE	Native plasmids of Fusobacterium nucleatum: characterization and						
				JOURNAL	Native plasmids of Fusobacterium nucleatum: characterization and						
				MEDLINE	use in development of genetic systems						
				PUBMED	J. Bacteriol.	182 (4), 1176-1180 (2000)					
				REFERENCE	10648549						
				AUTHORS	Kinder Haake, S.						
				TITLE	Direct Submission						
				JOURNAL	Submitted (14-JUN-1999) Periodontics, UCLA School of Dentistry,						
				FEATURES	Location/Qualifiers						
				SOURCE	10833 LeConte Avenue, Los Angeles, CA 90095-1668, USA						
					1. - "pFN1"						
					/mol-type="genomic DNA"						
					/strain="12230"						
					/db-xref="EAXON:851"						
					/plasmid="pFN1"						
					/note="Lower-respiratory tract clinical isolate from the						
					Wadsworth Anaerobe Laboratory, West Los Angeles Veterans						
					Affairs Medical Center"						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	288	100.0	AF159249	AF159249 Fusobacte
2	284.8	98.9	6281	AF022647 Fusobacte
3	81.2	28.2	38692	AC116919 Dicthyoste
4	80.2	27.8	33321	AC116986 Dicthyoste
5	78.8	27.4	88549	AC116924 Dicthyoste
6	78.4	27.2	105682	AC116957 Dicthyoste
7	77.6	26.9	110000	AC116957_0 Dicthyoste
C 8	77.4	26.9	302156	AC116977 Dicthyoste
C 9	77	26.7	156975	CR394534 Danio rer
C 10	76.2	26.5	110000	Continuation (2 of AX344566 Sequence
C 11	76.2	26.5	344980	AY04085 Dicthyoste
C 12	76	26.4	2781	AX344566 Sequence
C 13	75.8	26.3	10039	AC115599 Dicthyoste
C 14	75.8	26.3	125623	AC115599 Dicthyoste
C 15	75.8	26.3	266344	AC116956 Dicthyoste
C 16	75.8	26.3	273275	AE014828 Plasmidiu
C 17	75.4	26.2	105320	AC116920 Plasmidiu
C 18	75.4	26.2	178273	AC005308 Plasmidiu
C 19	75.4	26.2	250531	AE014845 Plasmidiu

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 56.0345 Seconds

Title: US-09-747-385-6_COPY_1_250
Perfect Score: 250
Sequence: 1 catataactttttgttt.....agccatataattaaaaat 250

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgmn2_6/pctodata/1/ina/5A_COMB.seq:
2: /cgmn2_6/pctodata/1/ina/5B_COMB.seq:
3: /cgmn2_6/pctodata/1/ina/6A_COMB.seq:
4: /cgmn2_6/pctodata/1/ina/6B_COMB.seq:
5: /cgmn2_6/pctodata/1/ina/PCTUS_COMB.seq:
6: /cgmn2_6/pctodata/1/ina/backfile1.seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
c 1	63	25.2	2447	2	US-09-014-969-14		Sequence 14, Appl1
c 2	61.6	24.6	396	4	US-09-640-173-53		Sequence 53, Appl1
c 3	61.6	24.6	396	4	US-09-713-550-53		Sequence 53, Appl1
c 4	61.6	24.6	396	4	US-09-825-294-53		Sequence 53, Appl1
c 5	61.6	24.6	396	4	US-09-970-966-53		Sequence 53, Appl1
c 6	61.2	24.5	1738	4	US-09-918-909A-27		Sequence 27, Appl1
c 7	59.2	23.7	240	1	US-08-628-411-6		Sequence 6, Appl1
c 8	59.2	23.3	1447	4	US-09-143-041A-27		Sequence 27, Appl1
c 9	58	23.2	8607	4	US-10-204-708-72		Sequence 72, Appl1
c 10	57.6	23.0	441	4	US-09-601-537-10		Sequence 9, Appl1
c 11	57.6	23.0	4121	4	US-09-601-537-9		Sequence 9, Appl1
c 12	57.2	22.9	2262	4	US-09-311-021-171		Sequence 171, Appl1
c 13	57	22.8	1474	3	US-08-811-994-64		Sequence 64, Appl1
c 14	56.8	22.7	2146	4	US-10-003-392-3		Sequence 3, Appl1
c 15	56.6	22.6	5152	4	US-10-204-708-47		Sequence 47, Appl1
c 16	56.2	22.5	396	4	US-09-640-173-33		Sequence 33, Appl1
c 17	56.2	22.5	396	4	US-09-713-550-33		Sequence 33, Appl1
c 18	56.2	22.5	396	4	US-09-925-294-33		Sequence 33, Appl1
c 19	56.2	22.5	396	4	US-09-966-33		Sequence 33, Appl1
c 20	56.2	22.5	1696	4	US-09-335-811-1		Sequence 1, Appl1
c 21	56	22.4	6409	4	US-09-167-998A-1		Sequence 1, Appl1
c 22	56	22.4	6409	4	US-10-159-151-1		Sequence 1, Appl1
c 23	55.8	22.3	7724	4	US-08-186-049-1		Sequence 1, Appl1
c 24	55.6	22.2	1117	3	US-09-247-373B-33		Sequence 33, Appl1
c 25	55.4	22.2	1985	4	US-09-307-794A-212		Sequence 212, Appl1
c 26	55.4	22.2	1985	4	US-09-115A-212		Sequence 212, Appl1
c 27	55.4	22.2	1985	4	US-09-902-775A-212		Sequence 212, Appl1

ALIGNMENTS

RESULT 1
US-09-014-969-14/C
; Sequence 14, Application US/09014969
; Parent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lawallie, Edward R.
; APPLICANT: Radic, Lisa A.
; APPLICANT: Moberg, David
; APPLICANT: Tracy, Maurice
; APPLICANT: Spaulding, Vicki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 87 Cambridge Park Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/014_969
; CLASSIFICATION:
; ATTN: SPRINGER, Suzanne A.
; NAME: SPRINGER, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5951
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-014-969-14

Query Match 63; DB 2; Length 2447;
Best Local Similarity 57.5%; Pred. No. 0.0014;
Matches 111; Conservative 1; Mismatches 81; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 264.607 Seconds

Title: US-09-747-385-6_COPY_1_250
Perfect score: 250 (without alignments)
Sequence: 1 catataataacttttgttt.....agccatataattaaaaat 250

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

N_Geneseqn23Sep04:
1: Geneseqn1980s:
2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002ab:
7: Geneseqn2002bs:
8: Geneseqn2003as:
9: Geneseqn2003bs:
10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004s:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
ABV40163/c
ID ABV40163 standard; cDNA; 556 BP.
XX AC ABV40163;
XX DT 16-SEP-2002 (first entry)
DB Human prostate expression marker cDNA 40154.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PP 20-FEB-2001; 2001WO-US005171.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	72.6	29.0	556 5 ABV40163	Abv40163 Human pro
c 2	72.6	29.0	556 5 ABV40063	Abv40063 Human pro
c 3	72.6	29.0	556 5 ABV42105	Abv42105 Human pro
c 4	72.6	29.0	556 5 ABV43601	Abv43601 Human pro
c 5	72.6	29.0	626 5 ABV60941	Abv60941 Human pro
c 6	71.2	28.8	277 8 ABX47508	Abx47508 Bovine ES
c 7	71.6	28.6	309 5 ABV44994	Abv44994 Human pro
c 8	70.2	28.1	375 5 ABV44911	Abv44911 Human pro
c 9	70.2	28.1	774 10 ADK57243	Adk57243 Plant DNA
c 10	68.2	27.3	9095 6 ABQ67061	Abq67061 Human ang
c 11	67.8	27.1	277 8 ABX47508	Abx47508 Bovine ES
c 12	67	26.8	310 4 AAH71505	Aah71505 Human cer
c 13	67	26.8	419 8 ABX46069	Abx46069 Bovine ES
c 14	66.8	26.7	1533 12 ADQ25148	Adq25148 Human sof
c 15	66.6	26.6	299 5 ADI72102	Adi72102 Human ova
c 16	66.6	26.6	299 5 ADL37251	Adl37251 Human ova
c 17	66.6	26.6	626 5 ABV60941	Abv60941 Human pro
c 18	66.6	26.6	2427 2 FAQ04107	Aaq04107 Human pro
c 19	65.8	26.3	545 4 AAH70126	Aah70126 Human cer
c 20	65.8	26.3	621 4 AAH71551	Aah71551 Human cer
c 21	65.6	26.2	494 5 ABV10021	Abv10021 Human pro

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the specification or its complement. (II) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the

AAC79727 Human sec
Add18806 Human dis
Aaf72806 Human dis
Abi12694 Human imm
Abx49849 Bovine ES
Aah70080 Human cer
Adi71997 Human ova
Adl37146 Human ova
Abx42739 Bovine ES
Abx47247 Bovine ES
Aai3197 Human pol
Adl37389 Human ova
Adi72244 Human ova
Abv38690 Human pro
Abg2014 Human pol
Adl10051 Cat flea
Abv16074 Human pro
Adl13389 Human ova
Abx39417 Bovine ES
Abx48619 Bovine ES
Abd13530 Human ova
Abx44057 Bovine ES
Adi43918 Human ova
Add22371 Human sof

ABQ9214 Human pol
Abv3197 Human pol
Abv16074 Human pro
Adl13389 Human ova
Abx39417 Bovine ES
Abx48619 Bovine ES
Abd13530 Human ova
Abx44057 Bovine ES
Adi43918 Human ova
Add22371 Human sof

ABQ9214 Human pol
Abv3197 Human pol
Abv16074 Human pro
Adl13389 Human ova
Abx39417 Bovine ES
Abx48619 Bovine ES
Abd13530 Human ova
Abx44057 Bovine ES
Adi43918 Human ova
Add22371 Human sof

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1214.56 Seconds (without alignments)

Title: US-09-747-385-6_COPY_1_250

Perfect score: 250

Sequence: 1 catataataacttttggtt.....agccatataattaaaaat 250

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 10%

Listing first 45 summaries

Database : GenBml:
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2: 9b_htg:/*
3: 9b_in:/*
4: 9b_on:/*
5: 9b_ov:/*
6: 9b_jpat:/*
7: 9b_ph:/*
8: 9b_jp1:/*
9: 9b_pr:/*
10: 9b_ro:/*
11: 9b_sts:/*
12: 9b_sy:/*
13: 9b_un:/*
14: 9b_vl:/*

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	FEATURES
1	250	100.0	5887	1	AF159249	AF159249 Fusobacterium nucleatum	AF159249 Fusobacterium nucleatum	Source
2	223	89.2	6281	1	AF022647	AF022647 Fusobacterium nucleatum	AF022647 Fusobacterium nucleatum	Source
c 3	72.6	29.0	556	6	C0508215	C0508215 Sequence	C0508215 Sequence	Source
c 4	72.6	29.0	556	6	C0508315	C0508315 Sequence	C0508315 Sequence	Source
c 5	72.6	29.0	556	6	C0510257	C0510257 Sequence	C0510257 Sequence	Source
c 6	72.6	29.0	556	6	C0511753	C0511753 Sequence	C0511753 Sequence	Source
c 7	71.8	29.0	626	6	C0529093	C0529093 Sequence	C0529093 Sequence	Source
c 8	71.8	28.7	227273	2	AC141526	AC141526 Rattus norvegicus	AC141526 Rattus norvegicus	Source
c 9	71.6	28.6	309	6	C0513146	C0513146 Sequence	C0513146 Sequence	Source
c 10	71.2	28.5	17756	2	CR318627	CR318627 Danio rerio	CR318627 Danio rerio	Source
c 11	70.8	28.3	12551	2	AC145940	AC145940 Strongylocephalus tenuirostris	AC145940 Strongylocephalus tenuirostris	Source
c 12	70.2	28.1	375	6	C0513063	C0513063 Sequence	C0513063 Sequence	Source
c 13	69.8	27.9	202872	2	AC016160	AC016160 Homo sapiens	AC016160 Homo sapiens	Source
c 14	69.4	27.8	11000	3	AC116984_1	AC116984_1 Continuation (2 of 2)	AC116984_1 Continuation (2 of 2)	Source
c 15	69.2	27.7	1373	10	BC049731	BC049731 Mus musculus	BC049731 Mus musculus	Source
c 16	69.2	27.7	1930	5	BC066725	BC066725 Danio rerio	BC066725 Danio rerio	Source
c 17	69	27.6	18871	3	AC117176	AC117176 Dictyostelia dictyostelia	AC117176 Dictyostelia dictyostelia	Source
c 18	68.8	27.5	28404	5	BX470087	BX470087 Zebrafish	BX470087 Zebrafish	Source
c 19	68.6	27.4	1946	5	BC077411	BC077411 Xenopus laevis	BC077411 Xenopus laevis	Source

ALIGNMENTS

RESULT 1 AF159249	LOCUS	AF159249	5887 bp	DNA	circular BCT 09-FEB-2000
	DEFINITION	Fusobacterium nucleatum plasmid pFNL			complete sequence.
	ACCESSION	AF159249			
	VERSION	AF159249.1	GI:6941824		
	KEYWORDS				
	SOURCE	Fusobacterium nucleatum			
	ORGANISM	Fusobacterium nucleatum			
		Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;			
		Fusobacterium.			
REFERENCE	AUTHORS	Kinder Haake,S. and Finegold,S.M.			
	TITLE	DNA sequence analysis of the Fusobacterium nucleatum plasmid, pFNL			
JOURNAL	J. Dent. Res.	78, 420 (1999)			
REFERENCE	AUTHORS	Kinder Haake,S. and Yoder,S.			
	TITLE	Transformation of Fusobacterium nucleatum by electroporation (Abstract #H-9)			
JOURNAL	Abstr. Gen. Meet. Am. Soc. Microbiol.	99, 331 (1999)			
REFERENCE	AUTHORS	Haake,S.K., Yoder,S.C., Attarian,G. and Podkaminer,K.			
	TITLE	Native Plasmids of Fusobacterium nucleatum: characterization and use in development of genetic systems			
JOURNAL	MDLINE	20115567			
PUBLMED	10648549				
REFERENCE	AUTHORS	Kinder Haake,S.			
	TITLE	Direct Submission (14-JUN-1999) Periodontics, UCLA School of Dentistry, 10833 Le Conte Avenue, Los Angeles, CA 90095-1668, USA			
JOURNAL	LOCATION/QUALIFIERS	1. .5887			
		/organism="Fusobacterium nucleatum"			
		/mol_type="Genomic DNA"			
		/strain="1230"			
		/db_xref="taxon:851"			
		/plasmid="pFNL"			
		/note="Lower-respiratory tract clinical isolate from the Wadsworth Anaerobe Laboratory, West Los Angeles Veterans Affairs Medical Center"			

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 nucleic - nucleic search, using sw model
 on: January 5, 2005, 10:02:48 ; Search time 2249.52 Seconds
 (without alignments)
 4049.721 Million cell updates/sec
 File: US-09-74-385-15_COPY_1_250
 Effect score: 250
 quence: 1 cacctgacggccgttagc.....ggttcacgtatggccatc 250
 Scoring table: IDENTITY_NUC
 GapOp 10.0 , Gapext 1.0
 searched: 32822875 seqs, 18219865908 residues
 al number of hits satisfying chosen parameters: 65645750
 AU251092 AU251092
 AU248437 AU248437
 BQ844002 1030040D0
 AU249975 AU249975
 CO641266 USDA-FP1
 AU247386 AU247386
 CB550392 MMPL00021-
 CB550481 MMPL0021-
 CB549779 MMPL0018-
 AV403811 AV403811-
 AV403921 AV403921-
 CB548636 MMPL0018-
 CB550005 MMPL0006-
 AV404405 AV404405-
 BUT24260 SJMBFC05
 AU249799 AU249799
 BO819196 1030076B0
 AU246979 AU246979
 AV405131 AV405131
 CB550355 MMPL0003-
 CB549815 MMPL0011-

ALIGNMENTS																																																																																																																																																							
RESULT 1 CD451062/c																																																																																																																																																							
LOCUS CD451062 mRNA linear EST 03-JUN-2005 DEFINITION USDA-PP 103109 Adult Alate Brown Citrus Aphid Toxoptera citricida ORGANISM CDNA Clone WHWTC-41_F12 5', mRNA sequence.																																																																																																																																																							
ACCESSION CD451062 VERSION CD451062.1 GI:31365802																																																																																																																																																							
KEYWORDS EST. SOURCE Toxoptera citricida (brown citrus aphid) TOXOPTERA CITRICIDA ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidoidea; Aphididae; Aphidini; Toxoptera.																																																																																																																																																							
REFERENCE Aphid biology. Expressed genes from alate Toxoptera citricida, the brown citrus aphid. AUTHORS Hunter W.B., Dang P.M., Bausher, M.G., Chaparro, J.X., McKendree, W., and Sinisterra, X.H. TITLE J. Insect Sci. 3 (23), 1-7 (2003) JOURNAL Contact: Wayne B. Hunter COMMENT US Horticultural Research Laboratory																																																																																																																																																							
FEATURES USDA - ARS 2001 South Rock Rd., Fort Pierce, FL 34945, USA Tel: (772) 462-5898 Fax: (772) 462-5986 Email: whunter@ushrl.ars.usda.gov source Seq primer: T3 Primer 1. . 500 Location/Qualifiers /organism="Toxoptera citricida" /mol_type="mRNA" /db_xref="taxon:223852" source /clone="WHWTC-41_F12" /sex="Mixed population" /tissue_type="Entire insect" /dev_stage="Adult Alate" /lab_host="XL1-Blue" source /note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2: XbaI; Toxoptera citricida (Kirkaldy); A high quality EST with at least 100 contiguous bases at Trace Tuner score of 20 or better." ORIGIN Query Match 100.0%; Score 250; DB 6; Length 500; Best Local Simililarity 100.0%; Pred. No. 1.5e-02; Indels 0; Matchers 250; Conservative 0; Mismatches 0;																																																																																																																																																							
Sequence processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries																																																																																																																																																							
est: * -abase : 1: gb_est1: 2: gb_est2: 3: gb_htc: 4: gb_est3: 5: gb_est4: 6: gb_est5: 7: gb_est6: 8: gb_gss1: 9: gb_gss2: *																																																																																																																																																							
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SUMMARIES																																																																																																																																																							
<table border="1"> <thead> <tr> <th>No.</th> <th>Query</th> <th>Match</th> <th>Length</th> <th>ID</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>250</td> <td>100.0</td> <td>500</td> <td>6 CD451062</td> <td>CD451062 USDA-PP 1</td> </tr> <tr> <td>2</td> <td>250</td> <td>100.0</td> <td>528</td> <td>9 CG808215</td> <td>CG808215 1118020D0</td> </tr> <tr> <td>3</td> <td>250</td> <td>100.0</td> <td>539</td> <td>9 CG801749</td> <td>CG801749 1118024B0</td> </tr> <tr> <td>4</td> <td>250</td> <td>100.0</td> <td>581</td> <td>1 AV403804</td> <td>AV403804 AV403804</td> </tr> <tr> <td>5</td> <td>250</td> <td>100.0</td> <td>584</td> <td>1 AV404063</td> <td>AV404063 AV404063</td> </tr> <tr> <td>6</td> <td>250</td> <td>100.0</td> <td>608</td> <td>1 AJ611113</td> <td>AJ611113 AJ611113</td> </tr> <tr> <td>7</td> <td>250</td> <td>100.0</td> <td>613</td> <td>1 AU250522</td> <td>AU250522 AU250522</td> </tr> <tr> <td>8</td> <td>250</td> <td>100.0</td> <td>614</td> <td>5 BO823788</td> <td>BO823788 1030112G0</td> </tr> <tr> <td>9</td> <td>250</td> <td>100.0</td> <td>625</td> <td>5 BO813491</td> <td>BO813491 1030112G0</td> </tr> <tr> <td>10</td> <td>250</td> <td>100.0</td> <td>627</td> <td>1 AV403988</td> <td>AV403988 AV403988</td> </tr> <tr> <td>11</td> <td>250</td> <td>100.0</td> <td>627</td> <td>1 AV404061</td> <td>AV404061 AV404061</td> </tr> <tr> <td>12</td> <td>250</td> <td>100.0</td> <td>627</td> <td>1 AV404091</td> <td>AV404091 AV404091</td> </tr> <tr> <td>13</td> <td>250</td> <td>100.0</td> <td>627</td> <td>1 AV404095</td> <td>AV404095 AV404095</td> </tr> <tr> <td>14</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403779</td> <td>AV403779 AV403779</td> </tr> <tr> <td>15</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403828</td> <td>AV403828 AV403828</td> </tr> <tr> <td>16</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403918</td> <td>AV403918 AV403918</td> </tr> <tr> <td>17</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403919</td> <td>AV403919 AV403919</td> </tr> <tr> <td>18</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403945</td> <td>AV403945 AV403945</td> </tr> <tr> <td>19</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403970</td> <td>AV403970 AV403970</td> </tr> <tr> <td>20</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV403997</td> <td>AV403997 AV403997</td> </tr> <tr> <td>21</td> <td>250</td> <td>100.0</td> <td>628</td> <td>1 AV404068</td> <td>AV404068 AV404068</td> </tr> <tr> <td>22</td> <td>250</td> <td>100.0</td> <td>629</td> <td>1 AV404061</td> <td>AV404061 AV404061</td> </tr> <tr> <td>23</td> <td>250</td> <td>100.0</td> <td>630</td> <td>1 CN582805</td> <td>BQ81996 1.030081D0</td> </tr> <tr> <td>24</td> <td>250</td> <td>100.0</td> <td>642</td> <td>7 CN582805</td> <td>CN582805 USDA-PP 1</td> </tr> </tbody> </table>		No.	Query	Match	Length	ID	Description	1	250	100.0	500	6 CD451062	CD451062 USDA-PP 1	2	250	100.0	528	9 CG808215	CG808215 1118020D0	3	250	100.0	539	9 CG801749	CG801749 1118024B0	4	250	100.0	581	1 AV403804	AV403804 AV403804	5	250	100.0	584	1 AV404063	AV404063 AV404063	6	250	100.0	608	1 AJ611113	AJ611113 AJ611113	7	250	100.0	613	1 AU250522	AU250522 AU250522	8	250	100.0	614	5 BO823788	BO823788 1030112G0	9	250	100.0	625	5 BO813491	BO813491 1030112G0	10	250	100.0	627	1 AV403988	AV403988 AV403988	11	250	100.0	627	1 AV404061	AV404061 AV404061	12	250	100.0	627	1 AV404091	AV404091 AV404091	13	250	100.0	627	1 AV404095	AV404095 AV404095	14	250	100.0	628	1 AV403779	AV403779 AV403779	15	250	100.0	628	1 AV403828	AV403828 AV403828	16	250	100.0	628	1 AV403918	AV403918 AV403918	17	250	100.0	628	1 AV403919	AV403919 AV403919	18	250	100.0	628	1 AV403945	AV403945 AV403945	19	250	100.0	628	1 AV403970	AV403970 AV403970	20	250	100.0	628	1 AV403997	AV403997 AV403997	21	250	100.0	628	1 AV404068	AV404068 AV404068	22	250	100.0	629	1 AV404061	AV404061 AV404061	23	250	100.0	630	1 CN582805	BQ81996 1.030081D0	24	250	100.0	642	7 CN582805	CN582805 USDA-PP 1
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Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES	
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c 4	250	100.0	3417	17	US-10-466-959-1	Sequence 1, Appl	
5	250	100.0	3417	18	US-10-466-960A-1	Sequence 1, Appl	
c 6	250	100.0	3450	15	US-10-222-026A-20	Sequence 20, Appl	
7	250	100.0	3497	16	US-10-420-529-11	Sequence 11, Appl	
8	250	100.0	3501	17	US-10-466-959-12	Sequence 2, Appl	
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c 11	250	100.0	3954	17	US-10-796-486-53	Sequence 53, Appl	
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GenCore version 5.1.6
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RESULT 1 US-10-796-486-56

; Publication US-10796486

; Application No. US20040171574A1

; GENERAL INFORMATION:

; APPLICANT: Morsev, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; TITLE OF INVENTION: COMPOSITIONS

; FILE REFERENCE: FC1052B

; CURRENT APPLICATION NUMBER: US-10-796-486

; CURRENT FILING DATE: 2004-03-08

; PRIORITY APPLICATION NUMBER: US-09-628-730

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SEQ ID NO: 56

; LENGTH: 3327

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: PGHRH1-297alal1522SK construct

US-10-796-486-56

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Best Local Similarity 100.0%; Pred. No. 2.5e-73;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2575 CACCTGACGGCCCTGTAGCGGCCATTAAGCGGCCGTTACGGCGAGCG 2634

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Db 2635 TGACGGCTACACTTGCAAGGCCCTAGGCCCTCTGCCTTCCTCCCTTC 2694

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 2	250	OM nucleic - nucleic search, using sw model	3369	4	US-09-628-730-48	Sequence 48, Appli
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c 5	250	Perfect score: 250	3656	1	US-09-628-730-8	Sequence 8, Appli
c 6	250	Sequence: 1 caccgtacgcgcctgtatgc...ggttcacgttgccatc 250	3688	1	US-09-628-730-9	Sequence 9, Appli
c 7	250	Scoring table: IDENTITY_NUC Gapov 10.0 , Gapext 1.0	3878	3	US-09-628-730-52	Sequence 53, Appli
c 8	250	Searched: 824507 seqs, 35539441 residues	3954	4	US-09-628-730-53	Sequence 57, Appli
c 9	250	Total number of hits satisfying chosen parameters: 1649014	3976	4	US-09-628-730-57	Sequence 49, Appli
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c 13	250	Listing First 45 summaries	4659	1	US-09-628-730-10	Sequence 10, Appli
c 14	250	Database : Issued Patents NA:*	4665	3	US-09-628-730-51	Sequence 7, Appli
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c 16	250	2: /cgtn2_6/prodata/1/ina/5B_COMB.seq;*	4665	3	US-09-628-730-53	Sequence 7, Appli
c 17	250	3: /cgtn2_6/prodata/1/ina/6A_COMB.seq;*	4665	3	US-09-628-730-57	Sequence 7, Appli
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c 20	250	6: /cgtn2_6/prodata/1/ina/backfile1.seq;*	4748	4	US-09-628-730-54	Sequence 4, Appli
c 21	250	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	4818	1	US-09-628-730-11	Sequence 11, Appli
c 22	250	SUMMARIES	4821	1	US-09-628-730-12	Sequence 12, Appli
c 23	250	Total number of hits satisfying chosen parameters: 1649014	4824	1	US-09-628-730-13	Sequence 13, Appli
c 24	250	Minimum DB seq length: 0	4886	4	US-09-628-730-4	Sequence 4, Appli
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ALIGNMENTS

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; Sequence 56, Application US/09628730
; Patient No. 67593313
; GENERAL INFORMATION:
; APPLICANT: Moresco, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628-730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PGHRH1-297Ala1522SK construct
US-09-628-730-56

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Best Local Similarity 100.0%; Pred. No. 1.e-64; Mismatches 0; Indels 0; Gaps 0;
Matches 250; Conservative 0;
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Db 2575 CACCTGAGCGCCCTGTAGGGCCATAAGGCCGCTCCTTCGCTTCCCTTC 120
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Db 2815 GTGGGCATC 2824

RESULT 2
US-09-628-730-48
; Sequence 48, Application US/09628730

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6											
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Post-processing: Minimum Match 0%												
Maximum Match 100%												
Listing first 45 summaries												
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RESULT 1												
CL121339												
LOCUS	CH121339 ISB1-80F23 T7.1 ISB1 Xenopus tropicalis genomic survey sequence.											
DEFINITION	ISB1-80F23 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-80F23,											
ACCESSION	CH121339											
VERSION	GI:40614974											
KEYWORDS	GSS.											
ORGANISM	Xenopus tropicalis (western clawed frog)											
SOURCE	Xenopus tropicalis; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodidae; Xenopus; Silurana.											
REFERENCE	1 (bases 1 to 971) Kremitzki, C., Carter, J.J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.											
AUTHORS	A physical map of the xenopus tropicalis genome Unpublished (2003)											
TITLE												
JOURNAL												
COMMENT	Contact: Richard K Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 75000 Std Error: 0.00 Seq primer: T7 TAATCGACTCACTATAAGGG Class: BAC ends BAC ends High quality sequence start: 15 High quality sequence stop: 604. Location/Qualifiers Source 1. .971 /organism="Xenopus tropicalis" /mol_type="genomic DNA" /db_xref="Exon:8364" /clone="ISB1-80F23" /clone_lab="ISB1" /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC library Segment 1." ORIGIN											
Query	CL121339 ISB1-80F2 AW494144 UI-M-BH3- CD284564 G39169_45 CB87095 HP07E4T CL756223 OR BB0112 CL581651 OB_Ba008 CL618511 OR_BB001 CL618532 OR_BB001 CL722627 OR_BB005 CL744977 OR_BB008 CL744978 OR_BB008 CL756924 OR_BB012 CL722626 OR_BB005 AG048138 Pan trogl AG12170 Pan trogl AG11570 Pan trogl AG05036 Pan trogl AG06570 Pan trogl AG071608 Pan trogl AG109476 Pan trogl AG133646 Pan trogl AG083734 Pan trogl AG097424 Pan trogl AG051058 Pan trogl											
Match	Query Match Score 190.2; DB 9; Length 971; Best Local Similarity 93.8%; Pred. No. 1.9e-45; Matches 198; Conservative 0; Mismatches 13; Indels 0; Gaps 0;											
QY	1 TTTCGAAAAGAGTGTAGCTCTGATCGGGCAAACAAACCCGCTGTTAGGGTGTT 60 91 TTTCGAAAAGAGTGTAGCTCTGATCGGGCAAACAAACCCGCTGTTAGGGTGTT 150											
Db	61 TTTCGAAAAGAGTGTAGCTCTGATCGGGCAAACAAACCCGCTGTTAGGGTGTT 120											
Qy	61 TTTCGAAAAGAGTGTAGCTCTGATCGGGCAAACAAACCCGCTGTTAGGGTGTT 120											
SUMMARIES												
Result No.	Score	Query	Match	Length	DB ID	Description						
1	190.2	74.3	971	9	CL121339	CL121339 ISB1-80F2 AW494144 UI-M-BH3- CD284564 G39169_45 CB87095 HP07E4T CL756223 OR BB0112 CL581651 OB_Ba008 CL618511 OR_BB001 CL618532 OR_BB001 CL722627 OR_BB005 CL744977 OR_BB008 CL744978 OR_BB008 CL756924 OR_BB012 CL722626 OR_BB005 AG048138 Pan trogl AG12170 Pan trogl AG11570 Pan trogl AG05036 Pan trogl AG06570 Pan trogl AG071608 Pan trogl AG109476 Pan trogl AG133646 Pan trogl AG083734 Pan trogl AG097424 Pan trogl AG051058 Pan trogl						
2	185.4	72.4	266	2	AV94744	CD284564 G39169_45 CB87095 HP07E4T CL756223 OR_BB0112 CL581651 OB_Ba008 CL618511 OR_BB001 CL618532 OR_BB001 CL722627 OR_BB005 CL744977 OR_BB008 CL744978 OR_BB008 CL756924 OR_BB012 CL722626 OR_BB005 AG048138 Pan trogl AG12170 Pan trogl AG11570 Pan trogl AG05036 Pan trogl AG06570 Pan trogl AG071608 Pan trogl AG109476 Pan trogl AG133646 Pan trogl AG083734 Pan trogl AG097424 Pan trogl AG051058 Pan trogl						
C	3	185.4	72.4	453	6	CD284564 G39169_45 CB87095 HP07E4T CL756223 OR_BB0112 CL581651 OB_Ba008 CL618511 OR_BB001 CL618532 OR_BB001 CL722627 OR_BB005 CL744977 OR_BB008 CL744978 OR_BB008 CL756924 OR_BB012 CL722626 OR_BB005 AG048138 Pan trogl AG12170 Pan trogl AG11570 Pan trogl AG05036 Pan trogl AG06570 Pan trogl AG071608 Pan trogl AG109476 Pan trogl AG133646 Pan trogl AG083734 Pan trogl AG097424 Pan trogl AG051058 Pan trogl						
C	4	185.4	72.4	514	6	CB87095 HP07E4T CL756223 OR_BB0112 CL581651 OB_Ba008 CL618511 OR_BB001 CL618532 OR_BB001 CL722627 OR_BB005 CL744977 OR_BB008 CL744978 OR_BB008 CL756924 OR_BB012 CL722626 OR_BB005 AG048138 Pan trogl AG12170 Pan trogl AG11570 Pan trogl AG05036 Pan trogl AG06570 Pan trogl AG071608 Pan trogl AG109476 Pan trogl AG133646 Pan trogl AG083734 Pan trogl AG097424 Pan trogl AG051058 Pan trogl						
C	5	185.4	72.4	514	9	CL756923	CL756923					
C	6	185.4	72.4	516	9	CL587651	CL587651					
C	7	185.4	72.4	516	9	CL618531	CL618531					
C	8	185.4	72.4	516	9	CL618532	CL618532					
C	9	185.4	72.4	516	9	CL722627	CL722627					
C	10	185.4	72.4	516	9	CL744977	CL744977					
C	11	185.4	72.4	516	9	CL744978	CL744978					
C	12	185.4	72.4	516	9	CL756924	CL756924					
C	13	185.4	72.4	517	9	CL722626	CL722626					
C	14	185.4	72.4	609	9	AG048138	AG048138					
C	15	185.4	72.4	616	9	AG124170	AG124170					
C	16	185.4	72.4	618	9	AG114570	AG114570					
C	17	185.4	72.4	619	9	AG054036	AG054036					
C	18	185.4	72.4	620	9	AG064570	AG064570					
C	19	185.4	72.4	621	9	AG071608	AG071608					
C	20	185.4	72.4	621	9	AG109476	AG109476					
C	21	185.4	72.4	626	9	AG133646	AG133646					
C	22	185.4	72.4	627	9	AG083734	AG083734					
C	23	185.4	72.4	627	9	AG097424	AG097424					
C	24	185.4	72.4	637	9	AG051058	AG051058					

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 57.3793 Seconds
(without alignments)
31/71.212 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955
Perfect score: 256
Sequence: 1 ttccggaaaagaggatgttag.....cacattccccgaaaaagtgc 256

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394411 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:
1: /cgm2_6/ptodata/1/ina/SA_COMB.seq:
2: /cgm2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:
6: /cgm2_6/ptodata/1/ina/backfile1.seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	186.4	72.8	1360	3 US-09-092-649B-81	Sequence 81, Appl
c 2	186.0	72.7	1360	3 US-09-092-649B-80	Sequence 80, Appl
c 3	186.0	72.7	3987	3 US-09-082-649B-83	Sequence 83, Appl
c 4	186.0	72.7	3987	3 US-09-082-649B-84	Sequence 84, Appl
c 5	186.0	72.7	7612	4 US-09-092-649B-82	Sequence 2, Appl
c 6	185.4	72.4	1905	1 US-08-594-469-9	Sequence 9, Appl
c 7	185.4	72.4	1905	2 US-08-906-957-9	Sequence 9, Appl
c 8	185.4	72.4	1947	3 US-09-025-769B-264	Sequence 264, App
c 9	185.4	72.4	1947	4 US-09-490-070A-264	Sequence 264, App
c 10	185.4	72.4	1947	4 US-09-490-153-264	Sequence 264, App
c 11	185.4	72.4	2422	1 US-07-857-106-5	Sequence 5, Appl
c 12	185.4	72.4	2462	4 US-09-490-445-5	Sequence 5, Appl
c 13	185.4	72.4	2686	4 US-09-785-269C-11	Sequence 11, Appl
c 14	185.4	72.4	2704	4 US-09-623-551-27	Sequence 27, Appl
c 15	185.4	72.4	2755	2 US-07-916-098A-7	Sequence 7, Appl
c 16	185.4	72.4	2839	4 US-09-809-517A-36	Sequence 36, Appl
c 17	185.4	72.4	2865	4 US-09-825-972-9	Sequence 9, Appl
c 18	185.4	72.4	2869	4 US-09-795-872-8	Sequence 8, Appl
c 19	185.4	72.4	2927	2 US-08-941-647A-1	Sequence 1, Appl
c 20	185.4	72.4	2927	3 US-09-142-481-14	Sequence 14, Appl
c 21	185.4	72.4	2939	1 US-08-119-512-2	Sequence 2, Appl
c 22	185.4	72.4	2939	1 US-08-448-015B-2	Sequence 2, Appl
c 23	185.4	72.4	2939	3 US-08-814-412-17	Sequence 17, Appl
c 24	185.4	72.4	2961	3 US-08-416-935-6	Sequence 6, Appl
c 25	185.4	72.4	2973	4 US-09-402-266B-17	Sequence 17, Appl
c 26	185.4	72.4	3003	6 5182260-18	Patent No. 5182260
c 27	185.4	72.4	3104	1 US-07-415-307A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-082-649B-81/c
; Sequence 81, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or Therapeutic Protocols
; FILE REFERENCE: C1039/NUMBER: US/09/082-649B
; CURRENT APPLICATION NUMBER: US/09/082-649B
; PRIORITY NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 81
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid DNA mutant Kanamycin resistance gene
US-09-082-649B-81

Query Match 72.8%; Score 186.4; DB 3; Length 1360;
Best Local Similarity 99.5%; Pred. No. 4.1e-48;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGGAAAAAGAGTGTAGTCCTGATCGGCAACAAACCCGCTGGTAGGGTTGGT 60
Db 1224 TTGGAAAGAGTGTAGTCCTGATCGGCAACAAACCCGCTGGTAGGGTTGGT 1165
Qy 61 TTTTTGTTGCAAGAGCAGATTAGCGCAGAAAAAGGATCTAACAGAACATCCCTTG 120
Db 1164 TTTTTGTTGCAAGAGCAGATTAGCGCAGAACAGGATCTAACAGAACATCCCTTG 1105
Qy 121 ATCTTTCATCGGGCTAGGGCTAGTGGAACGAAACTCACGTTAAGGATTGGTC 180
Db 1104 ATCTTTCATCGGGCTAGGGCTAGTGGAACGAAACTCACGTTAACGGATTGGTC 1045
RESULT 2

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 270.958 Seconds

Perfect score: 256

Title: US-09-747-385-15_COPY_9700_9955

Sequence: 1 ttccggaaaaaggatgttag.....cacatttcccgaaaaagtgc 256

Scoring table: IDENTITY_NUC Gapop 10.0 . Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqm1980s:*

2: Geneseqm1980s:*

3: Geneseqm2000s:*

4: Geneseqm2001as:*

5: Geneseqm2001bs:*

6: Geneseqm2002as:*

7: Geneseqm2002bs:*

8: Geneseqm2003as:*

9: Geneseqm2003bs:*

10: Geneseqm2003cs:*

11: Geneseqm2003ds:*

12: Geneseqm2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	256	100.0	4597	4 AAF24901	Aaf24901 Nucleotid	
2	256	100.0	8115	6 ABA97958	Aba97958 Lactic ac	
3	256	100.0	8115	6 ABA97959	Aba97959 Lactic ac	
4	189.8	74.1	5195	6 ADQ74554	Abq74554 Human Dev	
5	189.8	74.1	5195	12 ADM94427	Adm94427 Human dev	
6	189.8	74.1	5566	6 ABN86160	Abn86160 Nucleotid	
c	7	187.2	73.1	3851	12 ADP8054	Adp8054 Vector pd
c	8	187	73.0	1824	4 AAS41089	Aas41089 cDNA enco
c	9	187	73.0	1824	4 AAK57143	Aak57143 Human imm
c	10	186.8	73.0	6756	12 ADJ57431	Adj57431 Vector pa
c	11	186.8	73.0	6757	6 AAS20498	Aas20498 Expressio
c	12	186.5	72.9	5875	8 ABZ75111	Abz75111 VEGF expr
c	13	186.4	72.8	5742	6 AAS20504	Aas20504 Expressio
c	14	186.4	72.8	5742	12 ADJ57437	Adj57437 Vector py
c	15	186.4	72.8	10160	12 ADP84798	Adp84798 HIV subty
c	16	186.4	72.8	10186	12 ADP84796	Adp84796 Plasmid c
c	17	186.4	72.8	10198	12 ADP84799	Adp84799 HIV subty
c	18	186.2	72.7	5091	10 ADI39129	Adi39129 B. subtil
c	19	186.2	72.7	5091	12 ADO80519	Ado80519 Plasmid p
c	20	186.2	72.7	5091	12 ADO80585	Ado80585 Plasmid p
c	21	186.2	72.7	5091	12 ADO80330	Ado80330 Plasmid p

ALIGNMENTS

RESULT 1					
ID	AAFP24901 standard; DNA; 4597 BP.	XX	AAFP24901;	XX	DT 20-APR-2001 (first entry)
C	186.2 72.7 5076 12 ADI90417 Clostridi	37	186 72.7 5584 3 AAC5532	38	186 72.7 5584 10 ABZ8766
C	186.2 72.7 5076 12 ADI90417 Clostridi	33	186 72.7 4470 3 AAC5532	39	186 72.7 4470 10 ABZ8767
C	186.2 72.7 5076 12 ADI90417 Clostridi	34	186 72.7 4886 12 ADL50418	40	185.6 72.5 9830 3 AAA96220
C	186.2 72.7 5076 12 ADI90417 Clostridi	35	186 72.5 4892 9 ADA50329	41	185.6 72.4 10704 2 AAQ43846
C	186.2 72.7 5076 12 ADI90417 Clostridi	36	186 72.4 5076 12 ADI90417 Clostridi	42	185.4 72.4 478 8 ADC13870
C	186.2 72.7 5076 12 ADI90417 Clostridi	43	185.4 72.4 478 10 ADC13870	44	185.4 72.4 695 2 AAV63310
C	186.2 72.7 5076 12 ADI90417 Clostridi	45	185.4 72.4 941 12 ADO36316 Intracell	XX	OS Synthetic.
XX	XX	XX	XX	XX	PN WO200078358-A2.
XX	XX	XX	XX	XX	PR 18-JUN-1999; 99US-0140260P.
PD	PD	PD	PD	PD	PA (COLL-) COLLABORATIVE GROUP LTD.
XX	XX	XX	XX	XX	PA PT Chen W; PI
XX	XX	XX	XX	XX	DR WPI; 2001-071363/3-P.
XX	XX	XX	XX	XX	PR 19-JUN-2000; 2000WO-US016837.
PD	PD	PD	PD	PD	PT 28-DEC-2000.

The specification describes a microsphere comprising dihydrazide crosslinked to nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for treating a subject having myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.

Example 1; Page 36-38; 38pp; English.

The specification describes a microsphere comprising dihydrazide crosslinked to nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for increasing cardiac angiogenesis. They are also useful for treating haemophilia. The present sequence represents the plasmid pCDNA3.1/GS, into which is inserted a polynucleotide sequence which is

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	AX451319 Sequence
OM nucleic - nucleic search, using sw model	Search time 1243.71 Seconds (without alignment)	CQ794458 Sequence
Run on:	January 5, 2005, 10:02:48 ;	CQ794452 Sequence
Perfect score:	256	CQ795592 Sequence
Sequence:	1 ttccggaaaaaggatgttgttag.....cacatccccgaaaatgc 256	AX905091 Sequence
Scoring table:	IDENTITY_NUC Gapext 1.0	AX939595 Sequence
Searched:	US-09-747-385-15_COPY_9700_9955	CQB26646 Sequence
Total number of hits satisfying chosen parameters:	9053458	Q826647 Sequence
Minimum DB seq length:	0	Q826647 Sequence
Maximum DB seq length:	2000000000	Q795604 Sequence
Post-processing:	Maximum Match 0%	Q7945604 Shuttle v
	Listing first 45 summaries	AY265466 Shuttle v
Database :	GenEmbl:*	AY265466 Shuttle v
	1: gb_ba:*	AY265466 Shuttle v
	2: gb_htg:*	AY265466 Shuttle v
	3: gb_in:*	AY265466 Shuttle v
	4: gb_lm:*	AY265466 Shuttle v
	5: gb_ov:*	AY265466 Shuttle v
	6: gb_pat:*	AY265466 Shuttle v
	7: gb_ph:*	AY265466 Shuttle v
	8: gb_pl:*	AY265466 Shuttle v
	9: gb_pr:*	AY265466 Shuttle v
	10: gb_ro:*	AY265466 Shuttle v
	11: gb_sts:*	AY265466 Shuttle v
	12: gb_sy:*	AY265466 Shuttle v
	13: gb_un:*	AY265466 Shuttle v
	14: gb_vl:*	AY265466 Shuttle v
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
		SUMMARIES
Result No.	Query Score	Description
	Match	-----
	Length	-----
	DB ID	-----
1	256	X90639 Cloning vec
c 2	100.0	PCDNA3ZBO AF361441 Cloning v
c 3	100.0	PCDNA3ZBO AF361441 Cloning v
c 4	100.0	BD087749 Shuttle v
c 5	100.0	BD087750 Shuttle v
c 6	190	AY219688 Expression
c 7	189.8	AY219688 Expression
c 8	189.8	AY219688 Expression
c 9	187	AF102577 Cloning v
c 10	187	U14594 Shuttle vec
c 11	186.8	AC024392 Homo sapi
c 12	186.8	AC024392 Homo sapi
c 13	186.6	AC024392 Homo sapi
c 14	186.6	AC024392 Homo sapi
c 15	186.4	AC024392 Homo sapi
c 16	186.4	AC024392 Homo sapi
c 17	186.4	AC024392 Homo sapi
c 18	186.4	AC024392 Homo sapi
c 19	186.4	AC024392 Homo sapi
		Query Match 100.0% ; Score 256 ; DB 12 ; Length 3986 ; Best Local Similarity 100.0% ; Pred. No. 8 ; 1e-65 ; Matches 256 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ; ORIGIN 1 TTCGGAAAAAGAGTGTAGCTGATCCGGCAACAAACCGCTGGTAGCGTGGTGGT 60

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1168.43 Seconds
 (without alignments)

1 ttccggaaaaaggatgttgttag.....cacattcccggaaaagtgc 256

Title: US-09-747-385-15_COPY_9700_9955
 Perfect score: 256
 Sequence:

Total number of hits satisfying chosen parameters: 8352472

Scoring table: IDENTITY_NUC
 Gapox 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Published Applications NA:
 1: /cgn2_6/pctodata/2/pubpna/us07_PUBCOMB.seq:
 2: /cgn2_6/pctodata/2/pubpna/fct_new_pub.seq:
 3: /cgn2_6/pctodata/2/pubpna/us06_NEW_PUB.seq:
 4: /cgn2_6/pctodata/2/pubpna/us07_NEW_PUB.seq:
 5: /cgn2_6/pctodata/2/pubpna/bcrts_PUBCOMB.seq:
 6: /cgn2_6/pctodata/2/pubpna/us08_NEW_PUB.seq:
 7: /cgn2_6/pctodata/2/pubpna/us09_NEW_PUB.seq:
 8: /cgn2_6/pctodata/2/pubpna/us09A_PUBCOMB.seq:
 9: /cgn2_6/pctodata/2/pubpna/us09B_PUBCOMB.seq:
 10: /cgn2_6/pctodata/2/pubpna/us09C_PUBCOMB.seq:
 11: /cgn2_6/pctodata/2/pubpna/us09D_PUBCOMB.seq:
 12: /cgn2_6/pctodata/2/pubpna/us09_ENEW_PUB.seq:
 13: /cgn2_6/pctodata/2/pubpna/us10A_PUBCOMB.seq:
 14: /cgn2_6/pctodata/2/pubpna/us10B_PUBCOMB.seq:
 15: /cgn2_6/pctodata/2/pubpna/us10C_PUBCOMB.seq:
 16: /cgn2_6/pctodata/2/pubpna/us10D_PUBCOMB.seq:
 17: /cgn2_6/pctodata/2/pubpna/us10E_PUBCOMB.seq:
 18: /cgn2_6/pctodata/2/pubpna/us10_FNEW_PUB.seq:
 19: /cgn2_6/pctodata/2/pubpna/us11_NEWPUB.seq:
 20: /cgn2_6/pctodata/2/pubpna/us60_NEWPUB.seq:
 21: /cgn2_6/pctodata/2/pubpna/us60_PUBCOMB.seq:
 RESULT 1
 US-10-277-184-3
 ; Sequence 3, Application US/10277184
 ; Publication No. US20030114406A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, William
 ; TITLE OF INVENTION: HYALURONIC ACID MICROSPHERES FOR
 ; TREATMENT OF INVENTION: SUSTAINED GENE TRANSFER
 ; FILE REFERENCE: 2055_1IG717-US1
 ; CURRENT APPLICATION NUMBER: US/10/277,184
 ; CURRENT FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US/09/596,655
 ; PRIOR FILING DATE: 2000-06-19
 ; PRIORITY NUMBER: 60/140,260
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 4597
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: pCDNA3.1/GS vector by Invitrogen Corporation
 ; US-10-277-184-3

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	4597	15 US-10-277-184-3	Sequence 3, Appli
2	256	100.0	8115	9 US-09-778-516A-1	Sequence 1, Appli
3	256	100.0	8115	9 US-09-778-516A-2	Sequence 2, Appli
4	189.8	74.1	5195	16 US-10-419-045-2	Sequence 2, Appli
5	189.8	74.1	5566	15 US-10-400-053-22	Sequence 22, Appli
6	186.8	73.0	6757	9 US-09-896-594-16	Sequence 16, Appli
7	186.8	73.0	6757	16 US-10-185-415-16	Sequence 16, Appli
8	186.8	73.0	6757	16 US-10-672-484-16	Sequence 16, Appli
c 9	186.4	72.8	1360	11 US-09-165-101-81	Sequence 81, Appli
10	186.4	72.8	5742	9 US-09-836-594-22	Sequence 22, Appli
11	186.4	72.8	5742	16 US-10-185-415-22	Sequence 22, Appli
12	186.4	72.8	5742	16 US-10-672-484-22	Sequence 22, Appli